

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 8, 2003, 14:23:22 ; Search time 38 Seconds
(without alignments)
2955.149 Million cell updates/sec

Title: US-09-001-737-8

Perfect score: 2663

Sequence: 1 MAKEIKFSADARAAWYRGVD.....TPAPAMPAGMDPMWGMGNG 545

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_plant:*

10: sp_protist:*

11: sp_virus:*

12: sp_vertebrate:*

13: sp_viruses:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriophage:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2383.5	89.5	540	2	09AME7	09ame7 streptococ
2	2380	89.4	540	2	08VTS8	08vts8 streptococ
3	2347	88.1	540	16	097NV4	097nv4 streptococ
4	2333	87.6	481	2	033733	033733 streptococ
5	2330	87.5	540	2	02X4K5	02x4k5 streptococ
6	2199	82.4	541	2	03AE6	03ae6 enterococ
7	2185.5	82.1	541	2	03AE7	03ae7 streptococ
8	2015.5	75.8	539	2	03RC50	03rc50 bacillus sp
9	2011.5	75.5	539	2	08VW4	08vw4 bacillus th
10	2003.5	75.2	539	2	09EZY4	09ezy4 bacillus st
11	1999.5	75.1	544	2	032847	032847 lactobacill
12	1985	74.5	535	2	093G6	093g6 tetragenoco
13	1948	73.2	543	2	09KJ23	09kj23 lactobacill
14	1905	71.5	538	16	095EL7	095el7 staphylococ
15	1887	70.9	525	2	08VTW6	08vtw6 staphylococ
16	1877	70.5	525	2	08VTW8	08vtw8 staphylococ

17	1868.5	70.2	543	2	08RU00	08ru00 brevidacill
18	1850.5	69.5	546	2	093G07	093g07 lactobacill
19	1767.5	66.4	540	2	09KRF0	09krf0 clostridium
20	1759.5	66.1	540	2	09KJ77	09kj77 clostridium
21	1701.5	63.9	541	2	09KGM1	09kgm1 mycobacteri
22	1699	63.8	540	16	08RST7	08rst7 thermococ
23	1691.5	63.5	546	2	031198	031198 leptospira
24	1691.5	63.5	548	2	087888	087888 leishmania in
25	1690	63.5	551	16	098354	098354 rhizobium l
26	1687	63.3	548	16	09RW09	09rw09 delonococ
27	1681.5	63.1	539	16	08R5X7	08r5x7 streptococ
28	1672.5	62.8	541	16	09KXU5	09kxu5 streptococ
29	1668.5	62.7	537	2	09K171	09k171 bifidobacte
30	1664.5	62.5	546	2	08RT77	08rt77 xanthomonas
31	1661.5	62.4	546	16	08RBS3	08rbs3 brucella me
32	1660.5	62.4	546	2	093MH1	093mh1 rhodospirillum
33	1659.5	62.3	532	16	098AX9	098ax9 rhodococcus
34	1657	62.2	540	2	09KCA9	09kca9 rhodococcus
35	1657	62.2	542	2	09L691	09l691 rhizobium l
36	1657	62.2	549	16	0981J9	0981j9 rhizobium l
37	1655.5	62.2	538	2	09EY76	09ey76 bifidobacte
38	1654.5	62.1	533	2	09FDS2	09fds2 propionibac
39	1649.5	61.9	549	2	09AJB5	09ajb5 pseudomonas
40	1648	61.9	541	2	093Q12	093q12 corynebacte
41	1648	61.9	542	16	0981H9	0981h9 rhizobium l
42	1647.5	61.9	548	2	09L7P5	09l7p5 vibrio para
43	1645.5	61.8	545	2	093R08	093r08 enterococ
44	1644.5	61.8	538	2	09EZY1	09ezy1 thermococ
45	1642.5	61.7	560	16	08VTS8	08vts8 anabaena sp

ALIGNMENTS

RESULT 1

ID 09AME7 PRELIMINARY: PRT: 540 AA.

AC 09AME7: 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)

DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).

OS Streptococcus agalactiae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1311;

RN [1]

RP SEQUENCE FROM N.A.

RA Jwo-Farn C.;

RT "Cloning, sequencing, and characterization of 60 kDa Chaperonin gene from Streptococcus agalactiae."

RT Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).

CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

CC EMBL: AF35222; AK12938.1; ..

DR HSSP: P06139; IGRU.

DR InterPro: IPR001844; Chpnin_Cpn60.

DR InterPro: IPR002423; Cpn60_TCP-1.

DR Pfam: PF00118; Cpn60_TCP1.1.

DR PRINTS: PR00298; CHAPERONIN60.

DR PROSITE: PS00304; TCOMPLEXTCP1.

DR ATP-binding; Chaperone.

KW SEQUENCE 540 AA; 57287 MW; F392085FCF919ND1 CRC64;

Query Match 89.5%; Score 2383.5; DB 2; Length 540;
Best Local Similarity 89.7%; Pred. No 2.4e-105;
Matches 486; Conservative 25; Mismatches 26; Indels 3; Gaps 2;

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OY 1 MAKEIFSADARAAMVGVDMADTVKTLGPKGRNVYLEKAFSGSLITNDGVTIAKEIE 60
DB 1 MAKDIFSADARSAMVGVDMADTVKTLGPKGRNVYLEKAFSGSLITNDGVTIAKEIE 60
OY 61 LEHFEFNKAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
DB 61 LEHFEFNKAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
OY 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMENGVNDGVTIEESRG 180
DB 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMENGVNDGVTIEESRG 180
OY 181 METELEVEVGMOFDRGILSOYMTDNKEMVADLENPILITDKKVSINQIDILPLEEVLK 240
DB 181 METELEVEVGMOFDRGILSOYMTDNKEMVADLENPILITDKKVSINQIDILPLEEVLK 240
OY 241 TNRPLLIADVDGDEALPTLVNKRIGTFNVAVAKPGFDRRRAMLEDAITLGTGVIT 300
DB 241 TNRPLLIADVDGDEALPTLVNKRIGTFNVAVAKPGFDRRRAMLEDAITLGTGVIT 300
OY 301 EDLGLKDATMTALGOAKITVDKSTVIVEGSGSSAIAIRIALIKSOLLETTSDPDR 360
DB 301 EDLGLKDATMTALGOAKITVDKSTVIVEGSGSSAIAIRIALIKSOLLETTSDPDR 360
OY 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
DB 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
OY 421 IEKVALELEGGDAGTGRNIVYLALEEPYROIALNAGYSGSVYIDKLKNSPAGTGNATG 480
DB 421 IEKVALELEGGDAGTGRNIVYLALEEPYROIALNAGYSGSVYIDKLKNSPAGTGNATG 480
OY 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEVAVANKPEPATPAPAMPADMGKM 540
DB 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEVAVANKPEPATPAPAMPADMGKM 540
OY 541 GGM 543
DB 541 GGM 539

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RESULT 2

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OQ97S8 PRELIMINARY; PRT; 540 AA.
AC 08VTS8;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE GROEL.
OS Streptococcus gordonii.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1302;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC10558;
RA Teng L.-J, Hsu J.-C.;
RT "The groESL of Streptococcus gordonii ATCC 10558."
RL Submitted (JUN-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF382228; MAL73234.1;
DR InterPro: IPR001844; Chaperlin_Cpn60.
DR InterPro: IPR004423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1;
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR POSITIVE: PS00296; CHAPERONINS.CPN60; UNKNOWN.1.
SQ SOURCE 540 AA: 56769 MW: EAA47712767CE39 CRC64;
Query Match 89.4%; Score 2380; DB 2; Length 540;
Best Local Similarity 88.2%; Pred. No. 3,6e-105;
Matches 479; Conservative 39; Mismatches 21; Indels 4; Gaps 1;
OY 1 MAKEIFSADARAAMVGVDMADTVKTLGPKGRNVYLEKAFSGSLITNDGVTIAKEIE 60

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DB 1 MAKDIFSADARSAMVGVDMADTVKTLGPKGRNVYLEKAFSGSLITNDGVTIAKEIE 60
OY 61 LEHFEFNKAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
DB 61 LEHFEFNKAKLVSEVASKTNDIAGDGTATVTLQAIYHEGLKNTAGANPIGIRGIE 120
OY 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMENGVNDGVTIEESRG 180
DB 121 TATATVEALKAIQAPVSGKEALAOVAASRSREKVEYISEAMENGVNDGVTIEESRG 180
OY 181 METELEVEVGMOFDRGILSOYMTDNKEMVADLENPILITDKKVSINQIDILPLEEVLK 240
DB 181 METELEVEVGMOFDRGILSOYMTDNKEMVADLENPILITDKKVSINQIDILPLEEVLK 240
OY 241 TNRPLLIADVDGDEALPTLVNKRIGTFNVAVAKPGFDRRRAMLEDAITLGTGVIT 300
DB 241 TNRPLLIADVDGDEALPTLVNKRIGTFNVAVAKPGFDRRRAMLEDAITLGTGVIT 300
OY 301 EDLGLKDATMTALGOAKITVDKSTVIVEGSGSSAIAIRIALIKSOLLETTSDPDR 360
DB 301 EDLGLKDATMTALGOAKITVDKSTVIVEGSGSSAIAIRIALIKSOLLETTSDPDR 360
OY 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
DB 361 EKLQERLAKLVAGVAVIKVGAFTETALKEMKLRIEDALNATRAAVEGIVAGGTAITV 420
OY 421 IEKVALELEGGDAGTGRNIVYLALEEPYROIALNAGYSGSVYIDKLKNSPAGTGNATG 480
DB 421 IEKVALELEGGDAGTGRNIVYLALEEPYROIALNAGYSGSVYIDKLKNSPAGTGNATG 480
OY 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEVAVANKPEPATPAPAMPADMGKM 540
DB 481 EMDMKTGIIIDPKYKTRSAONASVASLITTEVAVANKPEPATPAPAMPADMGKM 540
OY 541 GGM 543
DB 541 GGM 539

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RESULT 3

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OQ97NV4 PRELIMINARY; PRT; 540 AA.
AC 097NV4;
DT 01-OCT-2001 (TREMblrel. 18, Created)
DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Chaperonin, 60 kDa (GROEL).
GN SP1906.
OS Streptococcus pneumoniae.
OC Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID-1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TIGR4;
RX MEDLINE-21357209; PubMed-11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Duxkan L.A., Gwin M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umeyan L.A., White O., Salzberg S.L., Lewis M.R., Redune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Ullrich T.R., Hansen C.B.,
RA McDonald L.A., Feldblyum T.V., Angluoi S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ESP174;
RA Dupoud D.F., Young A., Wright J.A.;
RT "Molecular chaperones/chaperonin-encoding stress genes groEL and groES

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Wed Apr 16 08:08:22 2003

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Page 3

RT and their use as antimicrobial targets.
BL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF007482; AAK75976.1;
DR EMBL: AF325449; AAL55997.1;
DR TIGR: SP1906;
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXCP1.
DR PROSITE: PS00296; CHAPERONIN_CPN60; 1.
KM Complete proteome.
SQ SEQUENCE 340 AA; 57095 MW; EBA6CB19C0CD894C CRC64;

Query Match 88.1%; Score 2347; DB 16; Length 540;
Best Local Similarity 87.8%; Pred. No. 1.3e-103;
Matches 477; Conservative 34; Mismatches 28; Indels 4; Gaps 1;

QY 1 MAKEIKFSADARAAMVGVMDLADTVKTLGPKGRNVYLEKAFGSLITNDGVTIAKEIE 60
D 1 MSKEIKFSADARAAMVGVMDLADTVKTLGPKGRNVYLEKAFGSLITNDGVTIAKEIE 60
D 61 LEDHFNNGAKLYSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPGRIGIE 120
D 61 LEDHFNNGAKLYSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPGRIGIE 120
QY 121 TATAVEALKAAQPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
D 121 TATAVEALKAAQPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
QY 121 TATAVEALKAAQPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
D 121 TATAVEALKAAQPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
QY 181 METELEVEGMOFDRGYLSQYMTDNEKNVADLENPELITLTKKVSNIODILEEVLK 240
D 181 METELEVEGMOFDRGYLSQYMTDNEKNVADLENPELITLTKKVSNIODILEEVLK 240
QY 241 TNRPLLIADVDGALPTVLNKRIGTFENVAAYAKAGFDRRKAMELIAITLGGTIVT 300
D 241 TNRPLLIADVDGALPTVLNKRIGTFENVAAYAKAGFDRRKAMELIAITLGGTIVT 300
QY 301 EDLGLKDATMTALGQAAKITVDKSTYIEGSGSEAIANRIALIKSOLETTTSDDPR 360
D 301 EDLGLKDATMTALGQAAKITVDKSTYIEGSGSEAIANRIALIKSOLETTTSDDPR 360
QY 361 EKLDERLAKIAGGVAVIKVAPETALKEMKLRIEDALNTRAAYEGSIYAGGTAITV 420
D 361 EKLDERLAKIAGGVAVIKVAPETALKEMKLRIEDALNTRAAYEGSIYAGGTAITV 420
QY 421 IEKVALEEGDDATGRIVLRALPEPQIALNAGEGSVYIDKLNSPAGTGFNAATG 480
D 421 IEKVALEEGDDATGRIVLRALPEPQIALNAGEGSVYIDKLNSPAGTGFNAATG 480
QY 481 EYVDMITGIIIDPVKVTRSALONAAVASLITTEAVANKKEPATAPAMPAGMDPGMM 540
D 481 EYVDMITGIIIDPVKVTRSALONAAVASLITTEAVANKKEPATAPAMPAGMDPGMM 540
QY 541 GGM 543
D 541 GGM 543
DB 537 GGM 539

RESULT 4

033733
ID 033733 PRELIMINARY; PRT: 481 AA.
AC 033733;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein) (Fragment).
GN GROEL.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1314;
RN [1]

RP SEQUENCE FROM N.A.
RA Pohl B., Podbelski A., Zarges I.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
DR EMBL: X89236; CAA61520.1;
DR HSP: P06139; IGR1.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60/TCF-1.
DR Pfam: PF00118; Cpn60_TCF1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXCP1.
DR PROSITE: PS00296; CHAPERONIN_CPN60; 1.
KM ATP-binding; Chaperone.
FT NON_TER
SQ SEQUENCE 481 AA; 50496 MW; FA80B97CA7B6D11 CRC64;

Query Match 87.6%; Score 2333; DB 2; Length 481;
Best Local Similarity 99.4%; Pred. No. 5.1e-103;
Matches 477; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 63 DHEFNNGAKLYSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPGRIGIE 122
D 1 DHEFNNGAKLYSEVASKTNDIAGDGTATVLTQAIYHEGLKNTAGANPGRIGIE 60
D 61 TATAVEALKAAQPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 182
D 61 TATAVEALKAAQPVSGKEAIAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 182
QY 183 TELEVEGMOFDRGYLSQYMTDNEKNVADLENPELITLTKKVSNIODILEEVLK 242
D 183 TELEVEGMOFDRGYLSQYMTDNEKNVADLENPELITLTKKVSNIODILEEVLK 242
QY 241 TNRPLLIADVDGALPTVLNKRIGTFENVAAYAKAGFDRRKAMELIAITLGGTIVT 302
D 241 TNRPLLIADVDGALPTVLNKRIGTFENVAAYAKAGFDRRKAMELIAITLGGTIVT 302
QY 301 EDLGLKDATMTALGQAAKITVDKSTYIEGSGSEAIANRIALIKSOLETTTSDDPR 362
D 301 EDLGLKDATMTALGQAAKITVDKSTYIEGSGSEAIANRIALIKSOLETTTSDDPR 362
QY 361 EKLDERLAKIAGGVAVIKVAPETALKEMKLRIEDALNTRAAYEGSIYAGGTAITV 422
D 361 EKLDERLAKIAGGVAVIKVAPETALKEMKLRIEDALNTRAAYEGSIYAGGTAITV 422
QY 421 IEKVALEEGDDATGRIVLRALPEPQIALNAGEGSVYIDKLNSPAGTGFNAATG 482
D 421 IEKVALEEGDDATGRIVLRALPEPQIALNAGEGSVYIDKLNSPAGTGFNAATG 482
QY 481 EYVDMITGIIIDPVKVTRSALONAAVASLITTEAVANKKEPATAPAMPAGMDPGMM 542
D 481 EYVDMITGIIIDPVKVTRSALONAAVASLITTEAVANKKEPATAPAMPAGMDPGMM 542
DB 421 VDMITGIIIDPVKVTRSALONAAVASLITTEAVANKKEPATAPAMPAGMDPGMM 480

RESULT 5

09X4R5
ID 09X4R5 PRELIMINARY; PRT: 540 AA.
AC 09X4R5;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
GN GROEL.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactob
OC Streptococcaceae; Streptococcus.
OX NCBI_Taxid=1313;
RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CP1200;
 RA Kim S.N., Lee J.Y., Kim S.W., Choi I.H., Rhee D.K.;
 RT "groEL" sequences in *Streptococcus pneumoniae*;
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
 CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
 CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
 CC CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
 CC 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR EMBL: AF117741; AAD3455.1; -
 DR HSPSP: P06139; IGRU.
 DR InterPro: IPR001844; Chaperonin_Cpn60.
 DR InterPro: IPR002423; Cpn60_TCP1.
 DR Pfam: PF00118; Cpn60_TCP1.
 DR PRINTS: PR00296; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEMENT1.
 DR PROSITE: PS00296; CHAPERONIN5_CPN60_1.
 DR ATP-binding; Chaperone.
 KM SEQUENCE 540 AA: 57213 MW: 4CDB489AF1C632DA CRC64;
 SQ
 Query Match 87.5%; Score 2330; DB 2; Length 540;
 Best Local Similarity 87.1%; Pred. No. 8,3e-103;
 Matches 473; Conservative 36; Mismatches 30; Indels 4; Gaps 1;
 QY 1 MAKEIKFSADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 DB 1 MSKEIKFSADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 QY 61 LEDHEFMGKLVSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 DB 61 LEDHEFMGKLVSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 QY 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 DB 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 QY 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 DB 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 QY 181 METELEVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 DB 181 METELEVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 QY 181 METELEVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 DB 181 METELEVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 QY 241 TNRPLLIADVDGALPTLVLNKIRGTFNVVAVKAPGDRRRKMLEDAIITGTYIT 300
 DB 241 SNRPLLIADVDGALPTLVLNKIRGTFNVVAVKAPGDRRRKMLEDAIITGTYIT 300
 QY 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 DB 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 QY 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 DB 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 QY 361 EKLOERLAKIAGVAVIKVGAFTETALKEMKLRIEDALNATRAVEGIVAGGCTALITV 420
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEMKLRIEDALNATRAVEGIVAGGCTALITV 420
 QY 361 EKLOERLAKIAGVAVIKVGAFTETALKEMKLRIEDALNATRAVEGIVAGGCTALITV 420
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEMKLRIEDALNATRAVEGIVAGGCTALITV 420
 QY 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 DB 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 QY 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 DB 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 QY 481 EWMVMKITGIIDPVKTVRSALONAAVSALLITTEAVVANKPEPATPAMPAGNDGGM 540
 DB 481 EWMVMKITGIIDPVKTVRSALONAAVSALLITTEAVVANKPEPATPAMPAGNDGGM 540
 QY 541 GGM 543
 DB 537 GGM 539
 RESULT 6
 Q93EUG PRELIMINARY; PRT: 541 AA.
 AC Q93EUG
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
 DE GROEL.
 GN Enterococcus faecalis (*Streptococcus faecalis*).
 OS Bacteria: Firmicutes: Bacillus/Clostridium group; Lactobacillales;
 OC Enterococaceae: Enterococcus.
 CX NCBI_TaxID=1351;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29212;
 RA Meng L.J., Tsuen P.R., Wang T.H., Lin H.M., Luh K.T., Ho S.W.;
 RT Determination of Enterococcus faecalis groEL full-length sequence
 RT and Application for Species Identification.
 RL J. Clin. Microbiol. 39:3326-3331(2001).
 DR EMBL: AF335185; AAL04033.1; -
 DR InterPro: IPR001844; Chaperonin_Cpn60.
 DR InterPro: IPR002423; Cpn60_TCP1.
 DR Pfam: PF00118; Cpn60_TCP1.
 DR PROSITE: PS00296; CHAPERONIN5_CPN60_1.
 DR ATP-binding; Chaperone.
 KM SEQUENCE 541 AA: 57052 MW: 6086A0C92075AB17 CRC64;
 SQ
 Query Match 82.4%; Score 2194; DB 2; Length 541;
 Best Local Similarity 81.7%; Pred. No. 2,3e-96;
 Matches 445; Conservative 46; Mismatches 48; Indels 6; Gaps 2;
 QY 1 MAKEIKFSADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 DB 1 MAKEIKFSADARAARAVRGVMDLADTVKVTLPGRKNVYLEKAFSGPLITNDGVTAKKE 60
 QY 61 LEDHEFMGKLVSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 DB 61 LEDHEFMGKLVSEVASKTNDIAGDGTATVTLQAIYHEGINKNTAGANPIGIRGIE 120
 QY 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 DB 121 TATATVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 QY 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 DB 122 TATAVAELKAIAPVSGKEAIAQVAAYSSRSKVEGYSISPMERVNGDVTIIESRG 180
 QY 181 METELEVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 DB 181 IETELDVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 QY 181 METELEVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 DB 181 IETELDVEGMPFDGYSIQYMTDENKVVADLENPFILITDKKYSNIODILPLEEVLK 240
 QY 241 TNRPLLIADVDGALPTLVLNKIRGTFNVVAVKAPGDRRRKMLEDAIITGTYIT 300
 DB 241 QSRPLLIADVDGALPTLVLNKIRGTFNVVAVKAPGDRRRKMLEDAIITGTYIT 300
 QY 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 DB 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 QY 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 DB 301 EDLGLKDATMTALGOAKITVDKSTVIYEGSGSEAIANRIALIKSOLETTSDPDR 360
 QY 361 EKLOERLAKIAGVAVIKVGAFTETALKEMKLRIEDALNATRAVEGIVAGGCTALITV 420
 DB 361 EKLOERLAKIAGVAVIKVGAFTETALKEMKLRIEDALNATRAVEGIVAGGCTALITV 420
 QY 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 DB 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 QY 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 DB 421 IEKVALELEGDDATGRNIVLRALPEPVROIALNAGYEGSVYIDKLKNSPAGTGFMAATG 480
 QY 481 EWMVMKITGIIDPVKTVRSALONAAVSALLITTEAVVANKPEPATPAMPAGNDGGM 540
 DB 481 EWMVMKITGIIDPVKTVRSALONAAVSALLITTEAVVANKPEPATPAMPAGNDGGM 540
 QY 541 GGM 545
 DB 536 -GNG 539
 RESULT 7
 Q9AEP7 PRELIMINARY; PRT: 542 AA.
 AC Q9AEP7
 DT 01-JUN-2001 (TREMblrel. 17, Created)

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01-JUN-2001 (Tremblrel. 17, last sequence update)
01-MAR-2002 (Tremblrel. 20, last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (GroEL protein).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales.
OC Streptococcaceae; Lactococcus.
OX NCBI_TaxId=1359;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-MG1363;
RA Vogensen F.K.; Kilstrup M.;
RT "groELs sequence from Lactococcus lactis subsp. cremoris MG1363."
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AY029215; AKK1639.1;
DR HSP: P06139; IGR1.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR Pfam: PF00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXCPI.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 542 AA; 57196 MW; EA81C4432EAFCA1 CRC64;

Query Match 82.1%; Score 2185.5; DB 2; Length 542;
Best Local Similarity 81.1%; Pred. No. 5,8e-96;
Matches 442; Conservative 49; Mismatches 49; Indels 5; Gaps 3;

OY 1 MAKEIFSADARAAMRGVMDLADYKVTGLGKGRNVYLEKFGSPPLITNDGYTIAKIE 60
DB 1 MSKEIFSSDANTAMRGIDILADVTGKTLGKGRNVYLEKSGSPPLITNDGYTIAKIE 60

OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVTOAIVHEGLKNTVAGANPIGIRGIE 120
DB 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVTOAIVHEGLKNTVAGANPIGIRGIE 120

OY 121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYISAMERGVNDGYTIEESRG 180
DB 121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYISAMERGVNDGYTIEESRG 180

OY 181 METELEVEEGMDFRGYLSQYVNTDNEKVAADLENPILITDKKYSNIDILPLEEVLK 240
DB 181 METELEVEEGMDFRGYLSQYVNTDNEKVAADLENPILITDKKYSNIDILPLEEVLK 240

OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGDFRRKAMLEDAITLTGTYIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGDFRRKAMLEDAITLTGTYIT 300

OY 301 EDGLLELKDNTATLGOAAKITYVDKSTVIYEGSGSESAIANRIALIKSOLETTSDDR 360
DB 301 EDGLLELKDNTATLGOAAKITYVDKSTVIYEGSGSESAIANRIALIKSOLETTSDDR 360

OY 361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGIVYAGGGATLTV 420
DB 361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGIVYAGGGATLTV 420

OY 421 IEKVAALTEEGDANTGRNIVLRALIEEPVROIALNAGYEGSVIIDLKNSAGCGNATG 480
DB 421 IEKVAALTEEGDANTGRNIVLRALIEEPVROIALNAGYEGSVIIDLKNSAGCGNATG 480

OY 481 EMDVMTKGTIDPYKVTYRSALQNAASVSLITTEAVANKEEPATAPMPAGDPCGM 540
DB 481 EMDVMTKGTIDPYKVTYRSALQNAASVSLITTEAVANKEEPATAPMPAGDPCGM 540

OY 541 GGMG 545
DB 541 GGMG 540

OY 537 -GMG 540
DB 537 -GMG 540

RESULT 8
OY 09RC20 PRELIMINARY; PRT: 539 AA.
AC 09RC20;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (GroEL protein).
GN Cpn60.
OS Bacillus sp. MS.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales.
OC Bacillaceae; Bacillus.
OX NCBI_TaxId=96470;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-MS.
RA Kondo A.; Yoshida M.;
RT Cpn60/10 from Bacillus strain MS.*;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AB028452; BAA88110.1;
DR HSP: P06139; IGR1.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PROSITE: PS00296; TCOMPLEXCPI.
KW ATP-binding; Chaperone.
SQ SEQUENCE 539 AA; 57346 MW; 95626C9080E30C46F CRC64;

Query Match 75.8%; Score 2019.5; DB 2; Length 539;
Best Local Similarity 74.7%; Pred. No. 4,2e-88;
Matches 407; Conservative 63; Mismatches 66; Indels 9; Gaps 2;

OY 1 MAKEIFSADARAAMRGVMDLADYKVTGLGKGRNVYLEKAGSPPLITNDGYTIAKIE 60
DB 1 MAKEIFSADARAAMRGVMDLADYKVTGLGKGRNVYLEKAGSPPLITNDGYTIAKIE 60

OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVTOAIVHEGLKNTVAGANPIGIRGIE 120
DB 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVTOAIVHEGLKNTVAGANPIGIRGIE 120

OY 121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYISAMERGVNDGYTIEESRG 180
DB 121 TATATVAEALKAIAQPVSGKEALIAQVAASRSSEKGEYISAMERGVNDGYTIEESRG 180

OY 181 METELEVEEGMDFRGYLSQYVNTDNEKVAADLENPILITDKKYSNIDILPLEEVLK 240
DB 181 METELEVEEGMDFRGYLSQYVNTDNEKVAADLENPILITDKKYSNIDILPLEEVLK 240

OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGDFRRKAMLEDAITLTGTYIT 300
DB 241 TNRPLLIADVDGEALPTLVNKRIGTFNVVAVKAPGDFRRKAMLEDAITLTGTYIT 300

OY 301 EDGLLELKDNTATLGOAAKITYVDKSTVIYEGSGSESAIANRIALIKSOLETTSDDR 360
DB 301 EDGLLELKDNTATLGOAAKITYVDKSTVIYEGSGSESAIANRIALIKSOLETTSDDR 360

OY 361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGIVYAGGGATLTV 420
DB 361 EKLQERLAKLAGVAIVKGAFTETALKEMLRIEDALNATRAAVEGIVYAGGGATLTV 420

OY 421 IEKVAALTEEGDANTGRNIVLRALIEEPVROIALNAGYEGSVIIDLKNSAGCGNATG 480
DB 421 IEKVAALTEEGDANTGRNIVLRALIEEPVROIALNAGYEGSVIIDLKNSAGCGNATG 480

OY 481 EMDVMTKGTIDPYKVTYRSALQNAASVSLITTEAVANKEEPATAPMPAGDPCGM 540
DB 481 EMDVMTKGTIDPYKVTYRSALQNAASVSLITTEAVANKEEPATAPMPAGDPCGM 540

OY 541 GGMG 545
DB 541 GGMG 540

OY 537 -GMG 540
DB 537 -GMG 540
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OY 481 EMDMKTGIDIPVKVTRSRALQNAASVALITTEAVANKPERPATPAMPAGNDPCM- 539
DB 481 EMDMKTGIDIPVKVTRSRALQNAASVALITTEAVANKPERPATPAMPAGNDPCM- 533
OY 540 -MGSM 543
DB 534 DMGSM 538

RESULT 9
OBYV84 PRELIMINARY: PRT: 539 AA.
AC 08V84:
DT 01-MAR-2003 (TREMblrel. 20, Created)
DT 01-MAR-2003 (TREMblrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE GROEL.
GN GROEL.
OS Bacillus thermoglucosidastus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Geobacillus.
OX NCBI_TaxID=1426;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-KP1006;
RX MEDLINE-21823396; PubMed-11834128;
RA Matanabe K., Fujiwara H., Inui K., Suzuki Y.;
RT "Oligo-1,6-glucosidase from a thermophile, Bacillus
thermoglucosidastus KP1006, was efficiently produced by combinatorial
RT expression of GROEL in Escherichia coli.";
RL Biotechnol. Appl. Biochem. 35:35-43(2002).
DR EMBL: AB025944; BAB83940.1;
DR InterPro: IPR001844; Chaperlin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; UNKNOWN_1.
SQ SOURCE 539 AA: 57192 MW: 7C5BE183F07C67B5 CRC64:

Query Match 75.5%: Score 2011.5; DB 2: Length 539;
Best Local Similarity 74.7%: Pred. No. 1e-87;
Matches 407; Conservative 62; Mismatches 67; Indels 9; Gaps 2;

OY 1 MAKEIFSADARAANVGVMDLADTVKTLGPKGRNVLEKAFGSPITNDGVTIAKEIE 60
DB 1 MAKEIFSADARAANVGVMDLADTVKTLGPKGRNVLEKAFGSPITNDGVTIAKEIE 60
OY 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLOAIHVGGLKNYAGANPIGRGIE 120
DB 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLOAIHVGGLKNYAGANPIGRGIE 120
OY 121 TATATVEMAKAIAOPVSGKEALIAQVAANVSSSEKGEVISEAMERVNDGVITIEESRG 180
DB 121 TATATVEMAKAIAOPVSGKEALIAQVAANVSSSEKGEVISEAMERVNDGVITIEESRG 180
OY 181 METELEVEGMOFRGVLISQYWTNDNEKVAADLENPFILITDKKVSNIQDILPLEEVLK 240
DB 181 METELEVEGMOFRGVLISQYWTNDNEKVAADLENPFILITDKKVSNIQDILPLEEVLK 240
OY 241 TNRPLLIADVDGEALPTLVNKLIRGTFFNVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
DB 241 TNRPLLIADVDGEALPTLVNKLIRGTFFNVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
OY 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALIANILILISOLETTSDPFR 360
DB 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALIANILILISOLETTSDPFR 360
OY 361 EELGRELKSTTIIASIGRASKVYVTKENTIVGAGDSERIKAINQINQAELESTSEFR 360
DB 361 EELGRELKSTTIIASIGRASKVYVTKENTIVGAGDSERIKAINQINQAELESTSEFR 360
OY 361 GILGRLAKLAGGVAVIKVGAFTALKEMKRIEDLANTRAVEEIVAGGCTALIV 420
DB 361 GILGRLAKLAGGVAVIKVGAFTALKEMKRIEDLANTRAVEEIVAGGCTALIV 420

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OY 421 IEKVALEEGDADGRNIVLRALPEYRQIALNAGYEGSVIDKLKNSPAGGFAATG 480
DB 421 YNKVALEAEGDEATGVIVLRAIEPYRQIAQNAAGLEGSIVLERKSGDIGFAATG 480
OY 481 EMDMKTGIDIPVKVTRSRALQNAASVALITTEAVANKPERPATPAMPAGNDPCM- 539
DB 481 EMDMKTGIDIPVKVTRSRALQNAASVALITTEAVANKPERPATPAMPAGNDPCM- 533
OY 540 -MGSM 543
DB 534 DMGSM 538

RESULT 10
OBYV84 PRELIMINARY: PRT: 539 AA.
AC 08V84:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE 60 kDa chaperonin (protein Cpn60) (GROEL protein).
GN GROEL.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC31783;
RA Sneydyan M., Gochikyan A., Weigel P., Sakanyan V.;
RT "Effect of thermostable chaperonins on synthesis of proteins in
RT vitro.";
RL SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL: AF274871; AAC44815.1;
DR HSSP: P06139; IGRL.
DR InterPro: IPR001844; Chaperlin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP-1.
DR Pfam: PF00118; Cpn60_TCP1.1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SOURCE 539 AA: 57293 MW: 2F51B6FFB887428 CRC64:

Query Match 75.2%: Score 2003.5; DB 2: Length 539;
Best Local Similarity 74.3%: Pred. No. 2.4e-87;
Matches 405; Conservative 63; Mismatches 68; Indels 9; Gaps 2;

OY 1 MAKEIFSADARAANVGVMDLADTVKTLGPKGRNVLEKAFGSPITNDGVTIAKEIE 60
DB 1 MAKEIFSADARAANVGVMDLADTVKTLGPKGRNVLEKAFGSPITNDGVTIAKEIE 60
OY 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLOAIHVGGLKNYAGANPIGRGIE 120
DB 61 LEDHFNNGAKLYEVASKTNDIAGDGTATATVLOAIHVGGLKNYAGANPIGRGIE 120
OY 121 TATATVEMAKAIAOPVSGKEALIAQVAANVSSSEKGEVISEAMERVNDGVITIEESRG 180
DB 121 TATATVEMAKAIAOPVSGKEALIAQVAANVSSSEKGEVISEAMERVNDGVITIEESRG 180
OY 181 METELEVEGMOFRGVLISQYWTNDNEKVAADLENPFILITDKKVSNIQDILPLEEVLK 240
DB 181 METELEVEGMOFRGVLISQYWTNDNEKVAADLENPFILITDKKVSNIQDILPLEEVLK 240
OY 241 TNRPLLIADVDGEALPTLVNKLIRGTFFNVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
DB 241 TNRPLLIADVDGEALPTLVNKLIRGTFFNVAVKAPGFGDRRKAMLEDAIILTGCVIT 300
OY 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALIANILILISOLETTSDPFR 360
DB 301 EDLGELEKDATATATLGOAAKITVDKSTIYVSGSSSEALIANILILISOLETTSDPFR 360
OY 361 EELGRELKSTTIIASIGRASKVYVTKENTIVGAGDSERIKAINQINQAELESTSEFR 360
DB 361 EELGRELKSTTIIASIGRASKVYVTKENTIVGAGDSERIKAINQINQAELESTSEFR 360
OY 361 GILGRLAKLAGGVAVIKVGAFTALKEMKRIEDLANTRAVEEIVAGGCTALIV 420
DB 361 GILGRLAKLAGGVAVIKVGAFTALKEMKRIEDLANTRAVEEIVAGGCTALIV 420

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OY 301 EDLGLKDATMTALGOAKITVDKDSVYVEGSSSEALANRLIKSOLETTSDPDR 360
 DB 301 EELGRELKSTTASIGRASVYVTEKNTTIEGACSDSIRAKRIQIADLETTSEDR 360
 OY 361 EKLQERLAKLAGVAVYKCAPTEALKEMLKRIEDALNTPAAVEGIVAGGCTALTIV 420
 DB 361 EKLQERLAKLAGVAVYKCAPTEALKEMLKRIEDALNTPAAVEGIVAGGCTALTIV 420
 OY 421 IEKVALELEGGDAGTGRNIVYRALPEEPQIALNAGIEGSSVYIDKLKNSPAGTGMAATG 480
 DB 421 YSKVAALIEAGDEATGVKIVYLAIEPEPQIALNAGIEGSSVYIDKLKNSPAGTGMAATG 480
 OY 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 539
 DB 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 539
 OY 540 -MGCM 543
 DB 534 DMGCM 538

RESULT 11

ID 032847 PRELIMINARY: PRT: 544 AA.
 AC 032847;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (GroEL protein).
 GN GROEL.
 OS Lactobacillus zeae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Lactobacillaceae; Lactobacillus.
 OX NCBI_TaxID-57037;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1025;
 RA Murphy C.M., Chassy B.M.;
 RT "Molecular Characterization of the Heat-Shock Regulated groESL operon of Lactobacillus zeae."
 RT Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases
 CC -1- FUNCTION: PREVENTS UNFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
 CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR EMBL: AC010281; AB06526.1; -;
 DR HSP: P06139; IGR1.
 DR Interpro: IPR001844; Chaperln-Cpn60.
 DR Interpro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1.1.
 DR PRINTS: PR00298; CHAPERONIN60.
 DR PRINTS: PR00304; TCOMPLEXTCP1.
 DR PROSITE: PS00296; CHAPERONINS_CPN60.1.
 DR ATP-binding; Chaperone.
 KW SEQUENCE 544 AA; 57428 MW; AA2F54AF4AC2A1AF CRC64;

Query Match 75.1% Score 1999.5; DB 2; Length 544;
 Best Local Similarity 74.1% Pred No. 3 Be-87;

Matches 404; Conservative 64; Mismatches 74; Indels 3; Gaps 2;

OY 1 MAKEITFSADARAAMRGVMDLADTVKVTGPGKRVNVEKAFSGPLITNDGVTIAKEIE 60
 DB 1 MAKEITFSADARAAMRGVMDLADTVKVTGPGKRVNVEKAFSGPLITNDGVTIAKEIE 60
 OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHEGLKANTVAGANPIGIRGIE 120
 DB 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHEGLKANTVAGANPIGIRGIE 120
 OY 121 TATATAVEALKAIAPVSGKEALIAQVAASRSSEKVGEXISEAMERGNQDGVITTEESRG 180
 DB 121 TATATAVEALKAIAPVSGKEALIAQVAASRSSEKVGEXISEAMERGNQDGVITTEESRG 180

DB 121 KATKANDELHKISRWKKEILQIAVAVSSSNTFVSLADAMEKVGHDGVITTEESRG 180
 OY 181 METELEVEVMQFDRGYLSQYVWTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
 DB 181 METELEVEVMQFDRGYLSQYVWTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
 OY 241 TRPPLIADVDGEALPTLVNKRIGTFNVAVAPGDFDRKAMLEIDIALIGCTVIT 300
 DB 241 OGRKALLIADVDGEALPTLVNKRIGTFNVAVAPGDFDRKAMLEIDIALIGCTVIT 300
 OY 301 EDLGLKDATMTALGOAKITVDKDSVYVEGSSSEALANRLIKSOLETTSDPDR 360
 DB 301 EDLGLKDATMTALGOAKITVDKDSVYVEGSSSEALANRLIKSOLETTSDPDR 360
 OY 361 EKLQERLAKLAGVAVYKCAPTEALKEMLKRIEDALNTPAAVEGIVAGGCTALTIV 420
 DB 361 EKLQERLAKLAGVAVYKCAPTEALKEMLKRIEDALNTPAAVEGIVAGGCTALTIV 420
 OY 421 IEKVALELEGGDAGTGRNIVYRALPEEPQIALNAGIEGSSVYIDKLKNSPAGTGMAATG 480
 DB 421 IEKVALELEGGDAGTGRNIVYRALPEEPQIALNAGIEGSSVYIDKLKNSPAGTGMAATG 480
 OY 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 540
 DB 481 EYVDMIKTGIIDPVKVTRSALONNAAVSALITTEAVVANKPEPATPAPAMPAGMDPGM 540
 OY 541 GCMG 545
 DB 538 AGMG 542

RESULT 12

ID 093GT6 PRELIMINARY: PRT: 535 AA.
 AC 093GT6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GROEL.
 GN GROEL.
 OS Tetragenococcus halophilus (Pediococcus halophilus).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Enterococcaceae; Tetragenococcus.
 OX NCBI_TaxID-51669;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Fukuda D., Watanabe M., Aso Y., Sonomoto K., Ishizaki A.;
 RT "The groESL operon of halophilic lactic acid bacterium Tetragenococcus halophilus."
 RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB073399; BAB70661.1; -;
 DR Interpro: IPR002423; Cpn60/TCF-1.
 DR Pfam: PF00118; Cpn60_TCF1.1.
 DR ATP-binding; Chaperone.
 KW SEQUENCE 535 AA; 56893 MW; D9FF681CD3A4D17C CRC64;

Query Match 74.5% Score 1985; DB 2; Length 535;
 Best Local Similarity 73.5% Pred No. 1 Be-86;
 Matches 396; Conservative 73; Mismatches 58; Indels 12; Gaps 2;

OY 1 MAKEITFSADARAAMRGVMDLADTVKVTGPGKRVNVEKAFSGPLITNDGVTIAKEIE 60
 DB 1 MAKEITFSADARAAMRGVMDLADTVKVTGPGKRVNVEKAFSGPLITNDGVTIAKEIE 60
 OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHEGLKANTVAGANPIGIRGIE 120
 DB 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQIVHEGLKANTVAGANPIGIRGIE 120
 OY 121 TATATAVEALKAIAPVSGKEALIAQVAASRSSEKVGEXISEAMERGNQDGVITTEESRG 180
 DB 121 TATATAVEALKAIAPVSGKEALIAQVAASRSSEKVGEXISEAMERGNQDGVITTEESRG 180
 OY 181 METELEVEVMQFDRGYLSQYVWTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240
 DB 181 METELEVEVMQFDRGYLSQYVWTDNEKNVADLENPILITDKVSNIDILPLEEVLK 240

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Db 177 IDLELVYGVGQDFRGYLSQYVWTDNEKMEADDSFYLLITDKRISMDIPLLEQVYV 236
Qy 241 TNRPLLIADVDGEALPTVYLNKIRGFENVVAVKPGFGRKRAKLEIDIALGGVIT 300
Db 237 ESKRPLIADIDGEALPTVYLNKIRGFENVVAVKPGFGRKRAKLEIDIALGGVIT 236
Qy 301 EDGELKDAITMTALGQAKITVDSDVYVEGSSSEAIANRIALIKSOLETTSPDR 360
Db 297 EDGELKDAITMTALGQAKITVDSDVYVEGSSSEAIANRIALIKSOLETTSPDR 356
Qy 361 EKLOERLAKLAGVAVIKVGAETELKEMKLEIDALNATRAAEEGIVAGGCTALTIV 420
Db 357 EKLOERLAKLAGVAVIKVGAETELKEMKLEIDALNATRAAEEGIVAGGCTALTIV 416
Qy 421 IEKVAALEEGDDA-TGRNIVYRALPEEVRQIALNAGYEGSVYIDKLKSPAGTFNATG 480
Db 417 INNVALLADDAITGVNIVYRALPEEVRQIALNAGYEGSVYIDKLKSEKIGIFENATG 476
Qy 481 EMDVMTKIGIIDPVKYVTSALONASVASLITTEVAANPEPATPAPAMPAGMDPM 539
Db 477 QMNVMDAGIVDPKYVTSALONASVASLITTEVAADPDPD-----ESGNDGV 527

RESULT 13
Qy 09KJ23 PRELIMINARY: PRT: 543 AA.
AC 09KJ23: 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein cpn60) (GroEL protein).
GN GROEL.
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Lactobacillaceae; Lactobacillus.
OX NCBI_TaxID=33959;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-VPI 11088; PubMed-10388700;
RX MEDLINE-9318659; Pubmed-10388700;
RA Walker D.C., Girgis H.S., Kleenhammer T.R.;
RT "The groEL chaperone operon of Lactobacillus johnsonii.";
RL Appl. Environ. Microbiol. 65:3033-3041(1999).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR HSP. P06139; IGR.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP1.
DR Pfam: PF00118; Cpn60_TCP1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00298; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONIN_CPN60; UNKNOWN_1.
KW ATP-binding; Chaperone.
SQ
SDQUENCE 543 AA: 57602 MW: BCEI6993JCD0638 CRC64;

Query Match 73.2%, Score 1948; DB 2; Length 543;
Best Local Similarity 73.1%, Pred. No. 1e-84;
Matches 397; Conservative 62; Mismatches 76; Indels 8; Gaps 3;

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Qy 121 TATAVEALKAAQPVSGKEATAOVAAVSSRSKGEVYISFAMRNQDGVITTEESRG 180
Db 121 TATAVADELHISIKSTKSTDELTAOVAAVSSRSKGEVYISFAMRNQDGVITTEESRG 180
Qy 181 METLEEVBEQDFDGYLSQYVWTDNEKMEADDSFYLLITDKRISMDIPLLEQVYV 240
Db 181 IDLELVYGVGQDFRGYLSQYVWTDNEKMEADDSFYLLITDKRISMDIPLLEQVYV 240
Qy 241 TNRPLLIADVDGEALPTVYLNKIRGFENVVAVKPGFGRKRAKLEIDIALGGVIT 300
Db 241 QGKSLIADVDGEALPTVYLNKIRGFENVVAVKPGFGRKRAKLEIDIALGGVIT 300
Qy 301 EDLELKDATMTALGQAKITVDSDVYVEGSSSEAIANRIALIKSOLETTSPDR 360
Db 301 SDLELKDATMTALGQAKITVDSDVYVEGSSSEAIANRIALIKSOLETTSPDR 360
Qy 361 EKLOERLAKLAGVAVIKVGAETELKEMKLEIDALNATRAAEEGIVAGGCTALTIV 420
Db 361 EKLOERLAKLAGVAVIKVGAETELKEMKLEIDALNATRAAEEGIVAGGCTALTIV 420
Qy 421 IEKVAALEEGDDA-TGRNIVYRALPEEVRQIALNAGYEGSVYIDKLKSPAGTFNATG 478
Db 421 MKSIGIVGDEDEAETGVYIKVKAAGAPVQIALNAGYEGSVYIDKLHEDPEVGTNAA 480
Qy 479 TGEVMDKIGIIDPVKYVTSALONASVASLITTEVAANPEPATPAPAMPAGMDPM 532
Db 481 TKNMNVKAGIIDPVKYVTSALONASVASLITTEVAADPDPD-----PATPAPAMP 540
Qy 533 AGM 535
Db 541 MGM 543

RESULT 14
Qy 099SL7 PRELIMINARY: PRT: 538 AA.
AC 099SL7: 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE 60 kDa chaperonin (Protein cpn60) (GroEL protein).
GN GROEL OR SA12029 OR SA1896.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcaceae; Staphylococcus.
OX NCBI_TaxID=158878; 158879;
RN (1)
RP SEQUENCE FROM N.A.
RC SPECIES-S. aureus (strain Mu50), and S. aureus (strain N315);
RX MEDLINE-21311952; Pubmed-11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Yamashita H., Kohara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Fuyuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR HSP. P06139; IGR.
DR InterPro: IPR001844; Chaperin_Cpn60.
DR InterPro: IPR002423; Cpn60_TCP1.
DR Pfam: PF00118; Cpn60_TCP1.

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DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONIN5_CPN60; 1.
DR ATP-binding; Chaperone; Complete proteome.
SQ SEQUENCE 538 AA; 57572 MW; A3D8595603DC9313 CRC64;

Query Match 71.5%; Score 1905; DB 16; Length 538;
Best Local Similarity 69.8%; Pred. No. 1,1e-82;
Matches 377; Conservative 78; Mismatches 83; Indels 2; Gaps 2;

OY 1 MAKEIKFSADARAAMVRCVMDLADTVKVTGAPGRNVYLEKAFSGSLITNDGVTIAKEIE 60
DB 1 MVKQKFSADARAAMVRCVMDLADTVKVTGAPGRNVYLEKAFSGSLITNDGVTIAKEIE 60
OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPIGIRGIE 120
DB 61 LEDPEFNMGAKLVSEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPIGIRGIE 120
OY 121 TATATAVEALKAIAQPVSGKEALAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
DB 121 TATATAVEALKAIAQPVSGKEALAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
OY 181 METELEVEEGMOPDRGYLSOYMTDNEKNVADLENPILITDKVSNIDILPLEEVK 240
DB 181 LNTLEVEVEGMOFDRGYLSOYMTDNEKNVADLENPILITDKVSNIDILPLEEVK 240
OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVAVKAPGFGDRRKAMLEDIALITGCVIT 300
DB 241 SNRPILIVADEVEGDALNTIYNLRMRGTFPAVAVKAPGFGDRRKAMLEDIALITGCVIT 300
OY 301 EDGLLEKDATMTALGOAKITVDKSTVIYEGSGSSEAIANRIALIKSOLETTSDPDR 360
DB 301 DDLGLDKDASIDMLGTASKVEVTKDNTVYDGDGSDNSIDARVSQLSIEETSDPDR 360
OY 361 EKLOERLAKLAGVAVIKVGAFTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
DB 361 EKLOERLAKLAGVAVIKVGAFTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
OY 421 IEKVAALEEGDDATGRNIVYLALEEPVROIALNAGYBSGVYIKLNSPATGNGATG 480
DB 421 YOKVSEIEAGDLEGGVNIYVLALEEPVROIALNAGYBSGVYIKLNSPATGNGATG 480
OY 481 EYDMIKTGIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 540
DB 481 EYVNMLEAGIVDPKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 540

RESULT 15

OBYTM6 PRELIMINARY; PRT; 525 AA.
AC 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE GroEL.
OS Staphylococcus aureus
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RN4220.
RA Dugourd D.F., Young A., Wright J.A.;
RT "Molecular chaperones/chaperonin-encoding stress genes groEL and groES
and their use as antimicrobial targets."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF325452; AAL56002.1;
DR InterPro; IPR001844; Chaprinin_Cpn60.
DR InterPro; IPR002423; Cpn60_TCP-1.
DR Pfam; PF00118; Cpn60_TCP1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCP1.
DR PROSITE; PS00296; CHAPERONIN5_CPN60; UNKNOWN_1.

SQ SEQUENCE 525 AA; 56209 MW; 6FDB2249E9878408 CRC64;

Query Match 70.9%; Score 1887; DB 2; Length 525;
Best Local Similarity 70.6%; Pred. No. 7.7e-82;
Matches 369; Conservative 78; Mismatches 76; Indels 0; Gaps 0;

OY 1 MAKEIKFSADARAAMVRCVMDLADTVKVTGAPGRNVYLEKAFSGSLITNDGVTIAKEIE 60
DB 1 MVKQKFSADARAAMVRCVMDLADTVKVTGAPGRNVYLEKAFSGSLITNDGVTIAKEIE 60
OY 61 LEDHEFNMGAKLVSEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPIGIRGIE 120
DB 61 LEDPEFNMGAKLVSEVASKTNDIAGDGTATATVLAQVYHEGLKNTAGANPIGIRGIE 120
OY 121 TATATAVEALKAIAQPVSGKEALAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
DB 121 TATATAVEALKAIAQPVSGKEALAOVAASRSSEKVEYISEAMERVNDGVITIEESRG 180
OY 181 METELEVEEGMOPDRGYLSOYMTDNEKNVADLENPILITDKVSNIDILPLEEVK 240
DB 181 LNTLEVEVEGMOFDRGYLSOYMTDNEKNVADLENPILITDKVSNIDILPLEEVK 240
OY 241 TNRPLLIADVDGEALPTLVNKRIGTFNVAVKAPGFGDRRKAMLEDIALITGCVIT 300
DB 241 SNRPILIVADEVEGDALNTIYNLRMRGTFPAVAVKAPGFGDRRKAMLEDIALITGCVIT 300
OY 301 EDGLLEKDATMTALGOAKITVDKSTVIYEGSGSSEAIANRIALIKSOLETTSDPDR 360
DB 301 DDLGLDKDASIDMLGTASKVEVTKDNTVYDGDGSDNSIDARVSQLSIEETSDPDR 360
OY 361 EKLOERLAKLAGVAVIKVGAFTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
DB 361 EKLOERLAKLAGVAVIKVGAFTETALKEMKRIEDALNSTRAAVEGIVAGGITALIV 420
OY 421 IEKVAALEEGDDATGRNIVYLALEEPVROIALNAGYBSGVYIKLNSPATGNGATG 480
DB 421 YOKVSEIEAGDLEGGVNIYVLALEEPVROIALNAGYBSGVYIKLNSPATGNGATG 480
OY 481 EYDMIKTGIIDPVKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 523
DB 481 EYVNMLEAGIVDPKVTRSALONASVASLITTEAVANKPEPATPAPAMPAGHDPM 523

Search completed: April 8, 2003, 14:26:06
Job time : 41 secs